

SEQUENCE LISTING

<110> Duvick, Jon

<120> Compositions and Methods for Fummonisin Detoxification

<130> 5718-111

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 1691

<212> DNA

<213> Exophiala spinifera

<220>

<223> flavin monooxygenase with intron

<400> 1

atgtcggcca ccagcaactc cagaggcgat tgttccgtcg catgcgacgc catcatcggt 60
ggagccggcc tcagcggcat ctctgctgtg tacaaattgc gaaagctcag actcaacgcc 120
aaaatcttcg agggagcccc cgattttggc ggcgtctggc actggaaccg ctaccctggc 180
gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
tggacctggt cttgccgcta tcctgaccag aaagagttgc tgcataatgt tcaccactgt 300
gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
tatgccagag atctgggacac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
aagtatctca ttctcgctac ggggttgctc cacaggaagc aactcccgcc actccccggc 480
ctcgcggatt tcaacgggaa ggtgattcat tcgagtgcct ggacgaaga cttcgacgca 540
gagggccaga gagtcgccc catcggtgcc ggggccacaa gcacccagat tgttcaggag 600
ttggccaaga aggtgacca ggtaaccatg tttatgcgaa ggccgagcta ttgtctgccc 660
atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctaccccaag 720
ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcggttggc 780
atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
gcctttaatt ttcttgcttg ccagtaccga gaagtcattg ttgacaaaaa ggccaaccga 900
ctgggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
gatctcatgg ctctcttgga gccgccgtac tggttcggta ccaagcgctc cccactggag 1020
agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
cccattgtgg ctgttacaaa gacaggtgtg ctcttgagtg acggcagcaa gagggaatgc 1140
gacacgatcg tgctggcgac gggtttcgac agtttccact gctcgtgagt gtgctcgatc 1200
atggctccga gtcgggacgt ttggctgacc ttgaaagatt gacacatatg ggcttgaaaa 1260
acaagcacgg agtggacctg aaggaggtgt ggaaagatgg catatctact tatatgggag 1320
tcttctctca tggcttcccc aatgccttct tcgtcgccac ggctcaagcc ccgaccgtcc 1380
tttccaacgg cccaacgatc atagaaaccc aagtcgactt gatcgccgat acaattgcaa 1440

agttggaggc cgagcacgcc acgtccgttg aggcgacgaa atcagcacia gaggcacgtt 1500
cgattatgat tgccaagatg aacgagcaca ctctgttccc cttgacggat tcgtggtgga 1560
ctggaggcaa catccctggg aaagcaacac gtgctttaac cttcataggc gggattgctc 1620
tctatgagca gatctgtcaa gagaaggtag ccaattggga tgggtttgat gtgcttcacg 1680
ctccctgcta a 1691

<210> 2

<211> 1638

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, fully spliced cDNA

<400> 2

atgtcggcca ccagcaactc cagaggcgat tgttccgtcg catgcgacgc catcatcggt 60
ggagccggcc tcagcggcat ctctgtgttg taaaaattgc gaaagctcag actcaacgcc 120
aaaatcttcg agggagcccc cgattttggc ggctgtctggc actggaaccg ctaccctggc 180
gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
tggacctggt cttgccgcta tctgaccag aaagagttgc tgcatatgt tcaccactgt 300
gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
aagtatctca ttctcgctac ggggttgctc cacaggaagc aactcccgcc actcccgccg 480
ctgcgcgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
gagggccaga gagtgcgcgt catcgggtgc ggggccacaa gcatccagat tgttcaggag 600
ttggccaaga aggtgacca ggtaaccatg tttatgcgaa ggccgagcta ttgtctgccc 660
atggggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctacccacg 720
ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcggttggc 780
atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
gcctttaatt ttcttgcttg ccagtaccga gaagtcattg ttgacaaaaa ggccaaccga 900
ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
gatctcatgg ctctctgga gccgcgtac tggttcggta ccaagcgtc cccactggag 1020
agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
cccattgtgg ctgttacaaa gacaggtgtg ctcttgagt acggcagcaa gagggaatgc 1140
gacacgatcg tgctggcgac gggtttcgac agtttactg gtcattgac acatatgggc 1200
ttgaaaaaca agcacggagt ggacctgaag gaggtgtgga aagatggcat atctacttat 1260
atgggagtct tctctcatgg cttccccaat gccttcttcg tcgccacggc tcaagccccg 1320
acogtccttt ccaacggccc aacgatcata gaaaccaag tcgacttgat cgccgatata 1380
attgcaaagt tggaggccga gcacgccacg tccgttgagg cgacgaaatc agcacaagag 1440
gcattggtcga ttatgattgc caagatgaac gagcacactc tgttcccctt gacggattcg 1500
tggtggactg gaggcaacat ccctgggaaa gcaacacgtg ctttaacctt cataggcggg 1560
attgctctct atgagcagat ctgtcaagag aaggtggcca attgggatgg gtttgatgtg 1620
cttcatgctc cctgctaa 1638

<210> 3

<211> 545

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, translation of fully spliced
cDNA

<400> 3

Met Ser Ala Thr Ser Asn Ser Arg Gly Asp Cys Ser Val Ala Cys Asp
1 5 10 15

Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys
20 25 30

Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
35 40 45

Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
50 55 60

Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
65 70 75 80

Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
85 90 95

Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
100 105 110

Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
115 120 125

Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile
130 135 140

Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly
145 150 155 160

Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
165 170 175

Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
180 185 190

Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
195 200 205

Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
210 215 220

Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr
225 230 235 240

Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala
245 250 255

Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr
260 265 270

Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln
275 280 285

Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp
290 295 300

Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg
305 310 315 320

Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg
325 330 335

Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val
340 345 350

Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr
355 360 365

Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val
370 375 380

Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly
385 390 395 400

Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly
405 410 415

Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe
420 425 430

Phe Val Ala Thr Ala Gln Ala Pro Thr Val Leu Ser Asn Gly Pro Thr
435 440 445

Ile Ile Glu Thr Gln Val Asp Leu Ile Ala Asp Thr Ile Ala Lys Leu
450 455 460

Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu
465 470 475 480

Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
 485 490 495

Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr
 500 505 510

Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys
 515 520 525

Gln Glu Lys Val Ala Asn Trp Asp Gly Phe Asp Val Leu His Ala Pro
 530 535 540

Cys
 545

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

<210> 4
 <211> 1464
 <212> DNA
 <213> Exophiala spinifera
 <220>
 <223> aldehyde dehydrogenase , fully spliced cDNA
 <400> 4

atggttcttt cgcctgacga atacaagagt gaactcttca tcaacaatga attcgtctcc 60
 tccaaggggt ccgagagatt aacgctcacg aaccggtggg acgaatccac cgttgccact 120
 gatgttcacg tggccaacgc ggccgatgtc gacagtgcag tagccgcttc ggtgcaggcg 180
 gtcaaaaagg gcccatggaa gaagttcaca ggtgcacaac gcgcggcggtg catgcttaag 240
 ttcgcgacc tcgccgagaa gaacgcgag aagctcgctc gtctggagtc gctgcccacc 300
 ggtagaccgg tgtcgatgat cactcatttc gacattccaa acatggtctc cgtgtttcgc 360
 tactatgcag gctgggcca caagatcgcc ggaaagacct ttcccaggga caacggcaag 420
 ccgaattggc gttacgagcc gatgggggtg tgtgctggtt ttgccagctg gaacgcgact 480
 tttctttacg tcggctggaa gatagcccc gccctcgccg ccggctgctc cttcatcttc 540
 aaagcctcgg agaaatcccc gctgggcgtt ctgggcctcg ctctctctt cgagaagcc 600
 ggattccctc ctggagtcgt gcagttcctc actggagcac gagtgcaggg tgaagcattg 660
 gcgtcgacac tggacattgc gaagatcagc ttcacaagat ctgtcgcgcg tggccgcgcc 720
 gtcaagcaag caacactcaa gtccaacatg aagcgctca ctctagaact gggggaaaag 780
 ccaaccatcg tcttcaacga agctcctctc gaacggcagt cgggggaatc ggcaaaggat 840
 ttctcaaaat tcgggcaaat ttgggtcccc cctcctggtt tgctagtgc atggggaaat 900
 ttagcggaga aattccatgg agtccgtcat ggctcatttg gaggctgtca gagatggctt 960
 ggccagaacc cattgaacc caagaggacg catggtccct tcgtcgacaa gtcccagtac 1020
 gacagagtct tgggtaacat tgacgttggc aaggataccg cgcagctcct cactggcggt 1080
 ggtagaaagg gcgacaaggg attcgcgatt gaaccgacga tatttgtcaa tcccaaacca 1140
 ggcagcaaaa tttggtttga ggagatcttt ggccccgtct tgtccattaa gacgttcaag 1200
 acggaagaag aggcatttga gattgccaat gacacgactt atgggctagc ctcggtcatt 1260
 tataccaaat ctctcaacag ggtctcctgt gtctcgctcg cgctcgagac cgttggcgctc 1320
 tcgatcaact tcccctttat ccccgagaca caaactccgt ttggcgcat gaaacaatcg 1380

ggctcaggca gagagctagg cgaagaaggg ctcaaggcgt acttgagacc caagaccatt 1440
aatatccacg tcaacataga gtga 1464

```
<210> 5
<211> 487
<212> PRT
<213> Exophiala spinifera
```

<220>
<223> aldehyde dehydrogenase, translation of fully
spliced cDNA

<400> 5
Met Val Leu Ser Pro Asp Glu Tyr Lys Ser Glu Leu Phe Ile Asn Asn
1 5 10 15

Glu Phe Val Ser Ser Lys Gly Ser Glu Arg Leu Thr Leu Thr Asn Pro
20 25 30

Trp Asp Glu Ser Thr Val Ala Thr Asp Val His Val Ala Asn Ala Ala
35 40 45

Asp Val Asp Ser Ala Val Ala Ala Ser Val Gln Ala Val Lys Lys Gly
50 55 60

Pro Trp Lys Lys Phe Thr Gly Ala Gln Arg Ala Ala Cys Met Leu Lys
65 70 75 80

Phe Ala Asp Leu Ala Glu Lys Asn Ala Glu Lys Leu Ala Arg Leu Glu
85 90 95

Ser Leu Pro Thr Gly Arg Pro Val Ser Met Ile Thr His Phe Asp Ile
100 105 110

Pro Asn Met Val Ser Val Phe Arg Tyr Tyr Ala Gly Trp Ala Asp Lys
115 120 125

Ile Ala Gly Lys Thr Phe Pro Glu Asp Asn Gly Lys Pro Asn Trp Arg
130 135 140

Tyr Glu Pro Met Gly Val Cys Ala Gly Ile Ala Ser Trp Asn Ala Thr
145 150 155 160

Phe Leu Tyr Val Gly Trp Lys Ile Ala Pro Ala Leu Ala Ala Gly Cys
165 170 175

Ser Phe Ile Phe Lys Ala Ser Glu Lys Ser Pro Leu Gly Val Leu Gly
180 185 190

Leu Ala Pro Leu Phe Ala Glu Ala Gly Phe Pro Pro Gly Val Val Gln
 195 200 205
 Phe Leu Thr Gly Ala Arg Val Thr Gly Glu Ala Leu Ala Ser His Met
 210 215 220
 Asp Ile Ala Lys Ile Ser Phe Thr Arg Ser Val Gly Gly Gly Arg Ala
 225 230 235 240
 Val Lys Gln Ala Thr Leu Lys Ser Asn Met Lys Arg Val Thr Leu Glu
 245 250 255
 Leu Gly Glu Lys Pro Thr Ile Val Phe Asn Glu Ala Pro Leu Glu Arg
 260 265 270
 Gln Ser Gly Glu Ser Ala Lys Asp Phe Ser Lys Phe Gly Gln Ile Trp
 275 280 285
 Val Pro Pro Ser Cys Leu Leu Val Gln Trp Gly Asn Leu Ala Glu Lys
 290 295 300
 Phe His Gly Val Arg His Gly Ser Phe Gly Gly Cys Gln Arg Trp Leu
 305 310 315 320
 Gly Gln Asn Pro Leu Glu Pro Lys Arg Thr His Gly Pro Phe Val Asp
 325 330 335
 Lys Ser Gln Tyr Asp Arg Val Leu Gly Asn Ile Asp Val Gly Lys Asp
 340 345 350
 Thr Ala Gln Leu Leu Thr Gly Val Gly Arg Lys Gly Asp Lys Gly Phe
 355 360 365
 Ala Ile Glu Pro Thr Ile Phe Val Asn Pro Lys Pro Gly Ser Lys Ile
 370 375 380
 Trp Phe Glu Glu Ile Phe Gly Pro Val Leu Ser Ile Lys Thr Phe Lys
 385 390 395 400
 Thr Glu Glu Glu Ala Ile Glu Ile Ala Asn Asp Thr Thr Tyr Gly Leu
 405 410 415
 Ala Ser Val Ile Tyr Thr Lys Ser Leu Asn Arg Gly Leu Arg Val Ser
 420 425 430
 Ser Ala Leu Glu Thr Gly Gly Val Ser Ile Asn Phe Pro Phe Ile Pro
 435 440 445

Glu Thr Gln Thr Pro Phe Gly Gly Met Lys Gln Ser Gly Ser Gly Arg
 450 455 460

Glu Leu Gly Glu Glu Gly Leu Lys Ala Tyr Leu Glu Pro Lys Thr Ile
 465 470 475 480

Asn Ile His Val Asn Ile Glu
 485

<210> 6
 <211> 1764
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <223> permease, partially spliced cDNA

<400> 6
 aactatggac tccagaccaa gtggatacgg cttgaaaggg gggacaaggc agacaacgaa 60
 gaacacagag acggcggcgg cagggtggtgc gtccgagtcg ctgaacgttc ctctggagaa 120
 gaaacaattt ggcaccatca ccatcggtgc cttggccttt gtgatttgca acagttgggc 180
 tggatctctc ggcagctctc agctcgccct actagcgggg gggcccgta ctctccttta 240
 cggcctccta atcagtactc tcgtctacat ctgcacgctt ttctcattag ccgaactgac 300
 cagcgtctac ccgactgccg gtggccaata tcattttgcg tcgacccctg caccaaaatc 360
 aatcaatcgg agcatttcat acgtgtgcgg actcgtgtcg ttgctttcat ggatcgctat 420
 cggaagctca gtgacctga tacctgctca acagatcccg gcgctgata ccgcctatag 480
 tcacacatac tcccaggatt cgtggcatgt cttcctcctc tacgagggag tcgcgctggt 540
 ggtgctcttg ttcaacttgt ttgccctgaa aagaaaccct tgggttcattg aaatcggatt 600
 cggcctcagc atcgctctct tcgtgatctc ctttatcgcc attctagcgc ggtccaaccc 660
 caaggctcca aactcacagg tatggactgc ttggagcaac tatactggct ggtccgacgg 720
 cgtctgcttc atcctggggc ttctgacatc ctgcttcatt ttcatggct tggacgcagc 780
 aatgcattct gctgaagaat gcacagatgc tgctcgtacg gtacccaaag cagtggctcag 840
 tgcaatcata attggcttct gcaccgcctt tccatataca atcgcagttc tgtatggaat 900
 tacagatctc gactctatto taagtccgcg cggctatatt ccattcgaga caatgaggca 960
 gtctgctcga attcggcttt ttgcaacggg cctctcatgt ggcggtatcg tgatggcctt 1020
 cttcgccctc aacgctgtac aagagactgc gtctcgactc acctggagct ttgcccggga 1080
 caatgggctg gtattttcca ctcatctcga acgcattcat ccccgctggc aagttcctgt 1140
 ttggtctcta ttcgcgacct ggggaattct ggccacatgc ggatgtatat ttctaggttc 1200
 tagcacagct ttcaatgcct tgggtcaatt cgcggttgta ctccagcaac tctccttcct 1260
 gatcccaatc gccctactcc tctacaaaaa gcgagatcca aagttcttgc cgagcactcg 1320
 tgctttttgt ttaccgcgtg gaatcgggtt tctgggtcaat gtgctagcgg tgggtcttcac 1380
 gtccgtcacc actgtgtttt tcagcttccc actgaccgtg cctacggccg cgtcaacat 1440
 gaattacaca agtgcgatta taggcgttgc acttgctctt ggtgtcttga actgggtcgt 1500
 gcatgccagg aagcattatc agggacccca cttggagctt gacggacggg tcgtcggagc 1560
 agaatttcaa gttgggccat gaattggacg aaatggagac gcgtgtgcaa tgtcaaaaat 1620
 tgctgggggtg gtactgagag tctggattag ctgcaacggg ggacaaccga gggtagaaca 1680

ctctgcaatc gagcaggaca atatcaatta ggcaachasv caaaaaaaaa aaaaaaaaaa 1740
 aaaaaagcgg ccgctgaatt ctag 1764

<210> 7
 <211> 1578
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <223> permease, fully spliced cDNA

<400> 7
 atggactcca gaccaagtgg atacggcttg aaaggcggga caaggcagac aacgaagaac 60
 acagagacgg cggcggcagg tgggtgcgtcc gagtcacctga acgttcctct ggagaagaaa 120
 caatttggca ccatacccat cgtgtccttg gcctttgtga ttgcaacag ttgggctggt 180
 atctcaggca gtctccagct cgccctacta gcgggggggc ccgtcactct cctttacggc 240
 atcctaataca gtactctcgt ctacatctgc atcgctttct cattagccga actgaccagc 300
 gtctacccga ctgcccgttg ccaatatcat tttgcgtoga tcctggcacc aaaatcaatc 360
 aatcggagca tttcatacgt gtgcggactc gtgtcgttgc tttcatggat cgctatcgga 420
 agctcagtga ccatgatacc tgctcaacag atcccggcgc tgatagccgc ctatagtcac 480
 acatactccc aggattcgtg gcatgtcttc ctcatctacg agggagtcgc gctgggtggtg 540
 ctcttgttca acttgtttgc cctgaaaaga aacccttggg ttcataaaat cggattcggc 600
 ctcacgacgt ctctcttctg gatctccttt atcgccattc tagcgcggtc caaccccaag 660
 gctccaaact cacaggatag gactgcttgg agcaactata ctggctggtc cgacggcgctc 720
 tgcttcatcc tgggcctttc gacatcctgc ttcattgttca ttggcttga cgcagcaatg 780
 catctggctg aagaatgcac agatgctgct cgtacggta ccaaagcagt ggtcagtgca 840
 atcataattg gcttctgcac cgcctttcca tatacaatcg cagttctgta tggaattaca 900
 gatctcgact ctattctaag ttccgcggc tatattccat tcgagacaat gaggcagtct 960
 gctcgaattc ggctttttgc aacggtcctc tcatgtggcg gtatcgtgat ggccttcttc 1020
 gccctcaacg ctgtacaaga gactgcgtct cgactcacct ggagctttgc ccgggacaat 1080
 gggctggtat tttccactca tctcgaacgc attcatcccc gctggcaagt tcctgtttgg 1140
 tctctattcg cgacctggg aattctggcc acatgcggat gtatatttct aggttctagc 1200
 acagctttca atgccttgg caattccgcc gttgtactcc agcaactctc ctctctgac 1260
 ccaatcgccc tactcctcta ccaaaagcga gatccaaagt tcttgccgag cactcgtgct 1320
 tttgtgttac cgcgtggaat cgggtttctg gtcaatgtgc tagcgggtgt cttcacgtcc 1380
 gtcaccactg tgtttttcag cttccactg accgtgccta cggccgcgtc aaccatgaat 1440
 tacacaagtg cgattatagg cgttgcaact gctcttgggt tcttgaactg ggtcgtgcat 1500
 gccaggaagc attatcagg accccacttg gagcttgacg gacgggtcgt cggagcagaa 1560
 tttcaagttg ggccatga 1578

<210> 8
 <211> 525
 <212> PRT
 <213> *Exophiala spinifera*

<220>
 <223> permease, translation of fully spliced cDNA

<400> 8

Met Asp Ser Arg Pro Ser Gly Tyr Gly Leu Lys Gly Gly Thr Arg Gln
1 5 10 15

Thr Thr Lys Asn Thr Glu Thr Ala Ala Ala Gly Gly Ala Ser Glu Ser
20 25 30

Leu Asn Val Pro Leu Glu Lys Lys Gln Phe Gly Thr Ile Thr Ile Val
35 40 45

Ser Leu Ala Phe Val Ile Cys Asn Ser Trp Ala Gly Ile Ser Gly Ser
50 55 60

Leu Gln Leu Ala Leu Leu Ala Gly Gly Pro Val Thr Leu Leu Tyr Gly
65 70 75 80

Ile Leu Ile Ser Thr Leu Val Tyr Ile Cys Ile Ala Phe Ser Leu Ala
85 90 95

Glu Leu Thr Ser Val Tyr Pro Thr Ala Gly Gly Gln Tyr His Phe Ala
100 105 110

Ser Ile Leu Ala Pro Lys Ser Ile Asn Arg Ser Ile Ser Tyr Val Cys
115 120 125

Gly Leu Val Ser Leu Leu Ser Trp Ile Ala Ile Gly Ser Ser Val Thr
130 135 140

Met Ile Pro Ala Gln Gln Ile Pro Ala Leu Ile Ala Ala Tyr Ser His
145 150 155 160

Thr Tyr Ser Gln Asp Ser Trp His Val Phe Leu Ile Tyr Glu Gly Val
165 170 175

Ala Leu Val Val Leu Leu Phe Asn Leu Phe Ala Leu Lys Arg Asn Pro
180 185 190

Trp Val His Glu Ile Gly Phe Gly Leu Thr Ile Ala Leu Phe Val Ile
195 200 205

Ser Phe Ile Ala Ile Leu Ala Arg Ser Asn Pro Lys Ala Pro Asn Ser
210 215 220

Gln Val Trp Thr Ala Trp Ser Asn Tyr Thr Gly Trp Ser Asp Gly Val
225 230 235 240

Cys Phe Ile Leu Gly Leu Ser Thr Ser Cys Phe Met Phe Ile Gly Leu
245 250 255

Asp	Ala	Ala	Met	His	Leu	Ala	Glu	Glu	Cys	Thr	Asp	Ala	Ala	Arg	Thr			
			260						265					270				
Val	Pro	Lys	Ala	Val	Val	Ser	Ala	Ile	Ile	Ile	Gly	Phe	Cys	Thr	Ala			
		275					280					285						
Phe	Pro	Tyr	Thr	Ile	Ala	Val	Leu	Tyr	Gly	Ile	Thr	Asp	Leu	Asp	Ser			
		290				295					300							
Ile	Leu	Ser	Ser	Ala	Gly	Tyr	Ile	Pro	Phe	Glu	Thr	Met	Arg	Gln	Ser			
305				310						315					320			
Ala	Arg	Ile	Arg	Leu	Phe	Ala	Thr	Val	Leu	Ser	Cys	Gly	Gly	Ile	Val			
				325					330					335				
Met	Ala	Phe	Phe	Ala	Leu	Asn	Ala	Val	Gln	Glu	Thr	Ala	Ser	Arg	Leu			
			340					345					350					
Thr	Trp	Ser	Phe	Ala	Arg	Asp	Asn	Gly	Leu	Val	Phe	Ser	Thr	His	Leu			
		355					360					365						
Glu	Arg	Ile	His	Pro	Arg	Trp	Gln	Val	Pro	Val	Trp	Ser	Leu	Phe	Ala			
		370				375					380							
Thr	Trp	Gly	Ile	Leu	Ala	Thr	Cys	Gly	Cys	Ile	Phe	Leu	Gly	Ser	Ser			
385				390					395						400			
Thr	Ala	Phe	Asn	Ala	Leu	Val	Asn	Ser	Ala	Val	Val	Leu	Gln	Gln	Leu			
			405					410					415					
Ser	Phe	Leu	Ile	Pro	Ile	Ala	Leu	Leu	Leu	Tyr	Gln	Lys	Arg	Asp	Pro			
		420					425						430					
Lys	Phe	Leu	Pro	Ser	Thr	Arg	Ala	Phe	Val	Leu	Pro	Arg	Gly	Ile	Gly			
		435					440					445						
Phe	Leu	Val	Asn	Val	Leu	Ala	Val	Val	Phe	Thr	Ser	Val	Thr	Thr	Val			
		450				455					460							
Phe	Phe	Ser	Phe	Pro	Leu	Thr	Val	Pro	Thr	Ala	Ala	Ser	Thr	Met	Asn			
465				470					475						480			
Tyr	Thr	Ser	Ala	Ile	Ile	Gly	Val	Ala	Leu	Ala	Leu	Gly	Val	Leu	Asn			
			485					490					495					
Trp	Val	Val	His	Ala	Arg	Lys	His	Tyr	Gln	Gly	Pro	His	Leu	Glu	Leu			
			500					505					510					

Asp Gly Arg Val Val Gly Ala Glu Phe Gln Val Gly Pro
515 520 525

<210> 9
<211> 3999
<212> DNA
<213> *Exophiala spinifera*

<220>
<223> p-glycoprotein, with introns

<400> 9
tatttsccat ctmckatgaa tggcagatga atcggagaaa cctcgaccaa accaagatgg 60
cagtgagtcg tcctcacacc ctccccaga aaaggaaacc gaaggcagta tttcagacta 120
tctacgaatc ttcagatatg cggacaaata cgactggact ctcaatgtca tcgcgctcat 180
ctgcgccatc ggatccgggg cttcccttcc tctgatgtcg atcatcttcg gtagcttcac 240
caacaagtgc aacaattaca attcgggcga cgggagtcct gaagcgttca aggccgatgt 300
ggatcatttc gtccctgtgggt togtctacct ctttattggg aagtttgtcc tcacgtacgt 360
ttccacggct gccattacca tttcagctat acgaaccact cgaactcttc gacgagtgtt 420
ccttgaatgc accttgccgc aagaggtctg gcatttcgac aagcagagca atggagcaat 480
cgccactcag gtcactacca atggcaaccg tatacaaaca ggtattgccg agaaattggt 540
ctttaccgtg caggcacttt caatgttctt ttctgcattt gtggtcgtt tggcgtctca 600
gtggaagcta gctttaatca ccattgtccg catccctgcc attttctctg tcaccggcat 660
ctgcatagca attgatgccg ctcaggaggc caggatcacc aggatctact caccgcgccg 720
tgtcctcgca gaagaagtct tatcatccat ccggacagtc catgctttct acgcccagaa 780
gaaaatggtc gaaaaatatg atgtcttttt gcagcaagca caccaagaag ggaagaagaa 840
atcgccaaat tatggggctt tgttctcaac tgagtacttt tgcatttacg ctgctatcgc 900
actgggcctt ttgggaaagg tttttcgcat gtatcagaat ggcgaggttg ccgacgttgg 960
caaagtcttt actgttgcc ttcggtcacc tttagcagcc acgtccatct caatgcttgc 1020
gccttcaggt tcagtcgttt accaacgccg catcttcggc ctccgaatta ttcagtatca 1080
ttgacaaacc caccgagctc gacccttctc gacccttttt ggaaagcagc cagagggctg 1140
cttaggtcaa attgagatcc aaaacctggc atttgccctac ccctcccagc catctgcca 1200
agtacttcca gatttcaact tgacaattcc agctggcaag acgacggccc tcgtcgggtc 1260
atcaggtagc ggcaaaagca caatggtcgg cttacttgaa cgggtggtatc tgcccagttc 1320
ggggaggata ttacttgatg ggttggaact gggacaatac aatgtgaaat ggctgagaag 1380
ccgcattcgc ctggttcaac aggaacctgt gttgtttcgt ggcacaatct tccagaacat 1440
tgccaacggg ttcatggatg agcaacgaga tctgcctcgc gaaaaacaaa tggagcttgt 1500
gcaaaaagct tgcaaaagcag caatgccgac gtgttcatta atgagcttcc gaacggttat 1560
gagactgaag ttggcgagcg agccggagcc ttgagtggag gtcaacaagc cgaattgcaa 1620
tcgcacgaag tatcatatcg gatccaaga tcctgttact cgatgaagct accagcgccc 1680
ttgacccgaa ggccggagaaa gtggtccagg aggccttgaa ccgagtgtcc aaagaccgca 1740
ctactttggt cattgcccac aaactagcca ctgtcatacg actcactatt agggcgaatt 1800
gggcccctcta gatgcatgct cgagcggccg ccagtgtgac gaattgatgc agaattcggc 1860
ttgtcattac gccgcactgg tgcgtgcaca ggacctcggg gctgacgaac aagaagaaca 1920
tgagaagacc ctgcacgaaa aggcagcacg agaagctgct ggtgaacgac cggcacttga 1980
gcgcactcac accactgcca catctcaagc tggagacctg gagaagcgga aggtgccggt 2040

cgggactttg ggctactcgc tcctaaaatg catcctaato atgttctacg aacaaaaaaa 2100
 tctctactgg tgcttcttgt tgtcaacaat agcgggttctg atatgcgcgg ccacatttcc 2160
 aggacaagcc cttttgtttt cgagattgct cactgtcttc gaggtagtg gtcattgcggc 2220
 acaggaacgg gcagactttt atagtctgat gttctttgtc gtggctctag gaaatctagt 2280
 aggatatttc acgattggct ggacatgcaa cgttgtttca caagttgtca cccatcgcta 2340
 tcgagccgaa atgttccaac gactactgga tcaagacatc gaattcttcg acatcccggg 2400
 gaatacttct ggtgctctca catcgcaact gtcagctcta cccacgcagt tgcaggagtt 2460
 gatatacaaa aattcttctc atttttatcg ttgtcgtaca acatcctctc gagcagtgct 2520
 ctagcactag cctatggatg gaaactgggc ctgggtggtg tggttggtgc acttccaccc 2580
 ctgcttttgg ctggctacct cagaattcgt cttgagacga agctagaagc cggaaactcg 2640
 gcaaaactttg cagaaagtgc tgggcttgca agcgaagcag ttaccgcgat cgggaccgtc 2700
 tcatctttga ctctcgaagg scatgttctc caacagtact cggacatgtt gagcaaggtc 2760
 gtgctaagat catccaaagc tttggtttgg acgatgtttt ggttctcact gtcacagtcg 2820
 atcgagtttc tggttatggc cctgggaatt ttggtatggg aagtcgacta ctggcttcag 2880
 gtgaggtacg acacaactca attttatatc atcttcgtgg gcgttttgtt tgccgggtcca 2940
 agcagcagcc cagaagccga attactccac gactcttacc aaggctcggg cggctgcgaa 3000
 ctatatcctc tggtcgcgga cattgaagcc gaccatccgc gaaacggagg agaacaagaa 3060
 aaaaaggcca gtgggtggat gccctgtcga cctcgaggac attgaattca ggtatcgtca 3120
 acgtgattcg gctcgagttc tccgcggggt ttccatgaca atcgagccag gacaatttgt 3180
 agcttatgtg ggcgcttctg gctgtggcaa gtcaacgttg atcgctttgt tggaacgatt 3240
 ctacgacccg acctcggggc gaatttcatt tgcacacgag aatattgcag aaatgtcgcc 3300
 gcgcttgtag cgcggccata tgtctttggt ccaacaggaa cccacayttt accaaggctc 3360
 cgttcgcgag aatgtgacgt tggccctcga agccgaatta tcagaagagc tttgtcaagg 3420
 acgccttccc gcaaggccaa tgctttggat tttgtcatct ctttaccaga aggccttgaa 3480
 acgccttgcg gctcaacgag ggatgcagtt ctccggcggg caacgacagc ggatcgccat 3540
 cgcaagagca ttgattcgaa atccaaagct gttgctactt gacgaagcga cgtcagccct 3600
 cgacacgcaa tcggaacgtc tggttcaagc tgccctcgat gaggcattca cgagccgaac 3660
 gacaatagca gtggcgcacc gactttccac tattcggaat gttgatgtta tttttgtgtt 3720
 tgccaacggg agaatcgccg aaacgggcac tcacgcggaa ctacaacgac tgagaggaa 3780
 atattacgag atgtgttttg cacaatcttt agaccaagca tgagcgttca cagagaagcg 3840
 gaaaagggcg gtgggatctt ttaggatagg tttagtggcg tgttacttac tacaggcggt 3900
 tggattcagg tacgacaact tgtacaataa gtatcataga gcatgtaatg aaagggtact 3960
 cgtcccggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3999

<210> 10

<211> 3792

<212> DNA

<213> Exophiala spinifera

<220>

<223> p-glycoprotein, fully spliced cDNA

<400> 10

atggcagatg aatcggagaa acctcgacca aaccaagatg gcagtgagtc gtcctcacac 60
 cctccccag aaaaggaaac cgaaggcagt atttcagact atctacgaat cttcagatat 120
 gccgacaaat acgactggac tctcaatgtc atcgcgctca tctgcgccat cggatccggg 180
 gcttcccttc ctctgatgtc gatcatcttc ggtagcttca ccaacaagtt caacaattac 240
 aattcgggag acgggagtc tgaagcgttc aaggccgatg tggatcatct cgtcctgtgg 300

ttcgtctacc tctttattgg gaagtttgtc ctcacgtacg tttccacggc tgccattacc 360
 atttcagcta tacgaaccac tcgaactcct cgacgagtgt tccttgaatg caccttgccg 420
 caagaggtct ggcatttcga caagcagagc aatggagcaa tcgccactca rgtcactacc 480
 aatggcaacc gtatacaaac aggtattgcc gagaaattgg tctttaccgt gcaggcactt 540
 tcaatgttct tttctgcatt tgtggtcgct ttggcgtctc agtggaaagt agctttaatc 600
 accatgtccg tcatccctgc cattttcctg gtcaccggca tctgcatagc aattgatgcc 660
 gctcaggagg ccaggatcac caggatctac tcacgcgcgc ctgtcctcgc agaagaagtc 720
 ttatcatcca tccggacagt ccattgcttc tacgcccaga agaaaatggc cgaaaaatat 780
 gatgtctttt tgcagcaagc acaccaagaa ggaagaaga aatcgccaaa taatgsgtc 840
 ttgttctcaa ctgagtactt ttgcatttac gctgctatcg cactggcctt ttggaaaggt 900
 tttcgcatgt atcagaatgg cgaggttgcc gacgttggca aagtctttac tgttgcctt 960
 tccgtcacct tagcagccac gtccatctca atgcttgcc cttcagggtc agtcgtttac 1020
 caacgccgca tcttcggctc cgaattattc agtatcattg acaaacccac gcagctcgac 1080
 cctctcgacc cttctggaaa gcagccagag ggctgcctag gtcaaattga gatccaaaac 1140
 ctggcatttg cctaccctc cggaccatct gcccaagtac ttcgagattt caacttgaca 1200
 attccagctg gcaagacgac ggccctcgtc ggtgcatcag gtagcggcaa aagcacaatg 1260
 gtcggcttac ttgaacggtg gtatctgccc agttcgggga ggatattact tgatgggttg 1320
 gaactgggac aatacaatgt gaaatggctg agaagccgca ttcgcctcgt tcaacaggaa 1380
 cctgtgttgt ttcgtggcac aatcttcag aacattgcca acggtttcat ggatgagcaa 1440
 cgagatctgc ctgcgaaaa acaaatggag cttgtgcaaa aagcttgcaa agccagcaat 1500
 ggcgacgtgt tcattaatga gcttcogaac ggttatgaga ctgaagttgg cgagcgagcc 1560
 ggagccttga gtggaggcca acgacaacga attgcaatcg cacgaagtat catatcggat 1620
 cccaagatcc tgttactcga tgaagctacc agcgccttg acccgaaggc ggagaaagtg 1680
 gtccaggagg ccttgaaccg agtgtccaaa gaccgcacta ctttggctcat tgcccacaaa 1740
 ctagccactg tcaaaagtgc tggcaacatc gcagtcattt cccaggggaa aatcgtcgag 1800
 caaggcacac accacgaatt gatcgaattc ggctgtcatt acgcccactt ggtgcgtgca 1860
 caggacctcg gggctgacga acaacaagaa catgagaaga ccctgcacga aaaggcagca 1920
 cgagaagctg ctggtgaacg accggcactt gagcgcactc acaccactgc cacatctcaa 1980
 gctggagacc tggagaagcg gaaggtgccg gtcgggactt tgggctactc gtccttaaaa 2040
 tgcacctaata tcatgttcta cgaacaaaaa aatctctact ggtgcttctt gttgtcaaca 2100
 ataacggttc tgatattgag ggcacattt ccaggacaag cccttttggt ttogagattg 2160
 ctactgtctc tcgagttgag tggctatgag gcacaggaac gggcagactt ttatattctg 2220
 atgttctttg tcgtggctct aggaaatcta gtaggatatt tcacgattgg ctggacatgc 2280
 aacgttattt cacaagttgt caccatcgc tatcaagccg caatgttcca acgagtactg 2340
 gatcaagaca tcgaactcct cgacatcccg gagcaaatct ctggtgctct cacatcgcaa 2400
 ctgtcagctc taccacgca gttgcaagag ttgatatcag caaattttct cttttatata 2460
 gttgtcggtc aacatcgtct cgagcagtgc tctaccacta gcctatggat ggaaactggg 2520
 cctgggtggt gtgttttggt cacttccacc cctgcttttg gctggctacc tcagaattcg 2580
 tctagagacg aagctagaag ccggaaaact ggcaaaactt gcagaaagtg ctgggcttgc 2640
 aagcgaagca gttaccgca tccggaccgt ctcatctttg actctogaag gccatgttct 2700
 ccaacagtac tcggacatgt tgagcaaggt cttgctaaga tcatccaaag ctttttggtt 2760
 ggacgatgtt ttggttttca cttgtcacag tcgatggagt ttttggctat tgccctggga 2820
 ttttgtattg cagtcgataa ttggcttcag gtgagtacga cacaactcaa ttttatatca 2880
 tottcgtggg cgttttggtt gccggtccaa gcagcagccc agtatttggc ttactccacg 2940
 agttttacca aggtcgggc ggctgcgaac tatatcctct ggctgcggac attgaagccg 3000
 accatccgag aaacggagga gaacaagaaa aaaggcccag tgggtggatg ccctgtcgac 3060
 ctcgaggaca ttgaattcag gtatcgtcaa cgtgattcgg ctcgagttct ccgcgggggt 3120
 tccatgacaa tcgagccagg acaatttgta gcttatgtgg gcgcttctgg ctgtggcaag 3180

tcaacgttga tcgctttgtc ggaacgattc tacgaccoga cctcggggcg aatttcattt 3240
gcacacgaga atattgcaga aatgtcgccg cgcttgtagc gcggccatat gtctttggtc 3300
caacaggaac ccacacttta ccaaggctcc gttcgcgaga atgtgacgtt ggccctcgaa 3360
gccgaattat cagaagagct ttgtcaagga cgccttcccg caaggccaat gctttggatt 3420
ttgtcatctc tttaccagaa ggctttgaaa cgccttgccg ctcaacgagg gatgcagttc 3480
tccggcgggc aacgacagcg gatcgccatc gcaagagcat tgattcgaaa tccaaagctg 3540
ttgtacttg acgaagcgac gtcagccctc gacacgcaat cggaacgtct ggttcaagct 3600
gccctcgatg aggcattccac gagccgaacg acaatagcag tggcgacccg actttccact 3660
attcggaatg ttgatgttat ttttgtgtt gccaacggga gaatcgccga aacgggcact 3720
cacgcggaac tacaacgact gagaggaaga tattacgaga tgtgtttggc acaatcttta 3780
gaccaagcat ga 3792

<210> 11

<211> 1263

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, translation of fully spliced cDNA

<400> 11

Met Ala Asp Glu Ser Glu Lys Pro Arg Pro Asn Gln Asp Gly Ser Glu
1 5 10 15

Ser Ser Ser His Pro Pro Pro Glu Lys Glu Thr Glu Gly Ser Ile Ser
20 25 30

Asp Tyr Leu Arg Ile Phe Arg Tyr Ala Asp Lys Tyr Asp Trp Thr Leu
35 40 45

Asn Val Ile Ala Leu Ile Cys Ala Ile Gly Ser Gly Ala Ser Leu Pro
50 55 60

Leu Met Ser Ile Ile Phe Gly Ser Phe Thr Asn Lys Phe Asn Asn Tyr
65 70 75 80

Asn Ser Gly Asp Gly Ser Pro Glu Ala Phe Lys Ala Asp Val Asp His
85 90 95

Phe Val Leu Trp Phe Val Tyr Leu Phe Ile Gly Lys Phe Val Leu Thr
100 105 110

Tyr Val Ser Thr Ala Ala Ile Thr Ile Ser Ala Ile Arg Thr Thr Arg
115 120 125

Thr Leu Arg Arg Val Phe Leu Glu Cys Thr Leu Arg Gln Glu Val Trp
130 135 140

His Phe Asp Lys Gln Ser Asn Gly Ala Ile Ala Thr Xaa Val Thr Thr
145 150 155 160

Asn Gly Asn Arg Ile Gln Thr Gly Ile Ala Glu Lys Leu Val Phe Thr
165 170 175

Val Gln Ala Leu Ser Met Phe Phe Ser Ala Phe Val Val Ala Leu Ala
180 185 190

Ser Gln Trp Lys Leu Ala Leu Ile Thr Met Ser Val Ile Pro Ala Ile
195 200 205

Phe Leu Val Thr Gly Ile Cys Ile Ala Ile Asp Ala Ala Gln Glu Ala
210 215 220

Arg Ile Thr Arg Ile Tyr Ser Arg Ala Ala Val Leu Ala Glu Glu Val
225 230 235 240

Leu Ser Ser Ile Arg Thr Val His Ala Phe Tyr Ala Gln Lys Lys Met
245 250 255

Val Glu Lys Tyr Asp Val Phe Leu Gln Gln Ala His Gln Glu Gly Lys
260 265 270

Lys Lys Ser Pro Asn Asn Gly Val Leu Phe Ser Thr Glu Tyr Phe Cys
275 280 285

Ile Tyr Ala Ala Ile Ala Leu Ala Phe Trp Lys Gly Phe Arg Met Tyr
290 295 300

Gln Asn Gly Glu Val Ala Asp Val Gly Lys Val Phe Thr Val Val Leu
305 310 315 320

Ser Val Thr Leu Ala Ala Thr Ser Ile Ser Met Leu Ala Pro Ser Gly
325 330 335

Ser Val Val Tyr Gln Arg Arg Ile Phe Gly Ser Glu Leu Phe Ser Ile
340 345 350

Ile Asp Lys Pro Thr Gln Leu Asp Pro Leu Asp Pro Ser Gly Lys Gln
355 360 365

Pro Glu Gly Cys Leu Gly Gln Ile Glu Ile Gln Asn Leu Ala Phe Ala
370 375 380

Tyr Pro Ser Arg Pro Ser Ala Gln Val Leu Arg Asp Phe Asn Leu Thr
385 390 395 400

Ile Pro Ala Gly Lys Thr Thr Ala Leu Val Gly Ala Ser Gly Ser Gly
405 410 415

Lys Ser Thr Met Val Gly Leu Leu Glu Arg Trp Tyr Leu Pro Ser Ser
420 425 430

Gly Arg Ile Leu Leu Asp Gly Leu Glu Leu Gly Gln Tyr Asn Val Lys
435 440 445

Trp Leu Arg Ser Arg Ile Arg Leu Val Gln Gln Glu Pro Val Leu Phe
450 455 460

Arg Gly Thr Ile Phe Gln Asn Ile Ala Asn Gly Phe Met Asp Glu Gln
465 470 475 480

Arg Asp Leu Pro Arg Glu Lys Gln Met Glu Leu Val Gln Lys Ala Cys
485 490 495

Lys Ala Ser Asn Gly Asp Val Phe Ile Asn Glu Leu Pro Asn Gly Tyr
500 505 510

Glu Thr Glu Val Gly Glu Arg Ala Gly Ala Leu Ser Gly Gly Gln Arg
515 520 525

Gln Arg Ile Ala Ile Ala Arg Ser Ile Ile Ser Asp Pro Lys Ile Leu
530 535 540

Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Pro Lys Ala Glu Lys Val
545 550 555 560

Val Gln Glu Ala Leu Asn Arg Val Ser Lys Asp Arg Thr Thr Leu Val
565 570 575

Ile Ala His Lys Leu Ala Thr Val Lys Ser Ala Gly Asn Ile Ala Val
580 585 590

Ile Ser Gln Gly Lys Ile Val Glu Gln Gly Thr His His Glu Leu Ile
595 600 605

Glu Phe Gly Cys His Tyr Ala Ala Leu Val Arg Ala Gln Asp Leu Gly
610 615 620

Ala Asp Glu Gln Gln Glu His Glu Lys Thr Leu His Glu Lys Ala Ala
625 630 635 640

Arg Glu Ala Ala Gly Glu Arg Pro Ala Leu Glu Arg Thr His Thr Thr
645 650 655

Ala Thr Ser Gln Ala Gly Asp Leu Glu Lys Arg Lys Val Pro Val Gly
660 665 670

Thr Leu Gly Tyr Ser Leu Leu Lys Cys Ile Leu Ile Met Phe Tyr Glu
675 680 685

Gln Lys Asn Leu Tyr Trp Cys Phe Leu Leu Ser Thr Ile Thr Val Leu
690 695 700

Ile Cys Ala Ala Thr Phe Pro Gly Gln Ala Leu Leu Phe Ser Arg Leu
705 710 715 720

Leu Thr Val Phe Glu Leu Ser Gly His Ala Ala Gln Glu Arg Ala Asp
725 730 735

Phe Tyr Ile Leu Met Phe Phe Val Val Ala Leu Gly Asn Leu Val Gly
740 745 750

Tyr Phe Thr Ile Gly Trp Thr Cys Asn Val Ile Ser Gln Val Val Thr
755 760 765

His Arg Tyr Gln Ala Ala Met Phe Gln Arg Val Leu Asp Gln Asp Ile
770 775 780

Glu Leu Leu Asp Ile Pro Glu Gln Ile Ser Gly Ala Leu Thr Ser Gln
785 790 795 800

Leu Ser Ala Leu Pro Thr Gln Leu Gln Glu Leu Ile Ser Ala Asn Phe
805 810 815

Leu Ile Tyr Ile Val Val Gly Gln His Arg Leu Glu Gln Cys Ser Thr
820 825 830

Thr Ser Leu Trp Met Glu Thr Gly Pro Gly Gly Cys Val Trp Cys Thr
835 840 845

Ser Thr Pro Ala Phe Gly Trp Leu Pro Gln Asn Ser Ser Arg Asp Glu
850 855 860

Ala Arg Ser Arg Lys Leu Gly Lys Leu Cys Arg Lys Cys Trp Ala Cys
865 870 875 880

Lys Arg Ser Ser Tyr Arg Asp Pro Asp Arg Leu Ile Phe Asp Ser Arg
885 890 895

Arg Pro Cys Ser Pro Thr Val Leu Gly His Val Glu Gln Gly Leu Ala
900 905 910

660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910

Lys Ile Ile Gln Ser Phe Trp Phe Gly Arg Cys Phe Gly Phe His Leu
 915 920 925

Ser Gln Ser Met Glu Phe Leu Ala Ile Ala Leu Gly Phe Cys Ile Ala
 930 935 940

Val Asp Asn Trp Leu Gln Val Ser Thr Thr Gln Leu Asn Phe Ile Ser
 945 950 955 960

Ser Ser Trp Ala Phe Cys Leu Pro Val Gln Ala Ala Ala Gln Tyr Leu
 965 970 975

Ala Tyr Ser Thr Ser Phe Thr Lys Ala Arg Ser Ala Ala Asn Tyr Ile
 980 985 990

Leu Trp Leu Arg Thr Leu Lys Pro Thr Ile Arg Glu Thr Glu Glu Asn
 995 1000 1005

Lys Lys Lys Gly Pro Val Gly Gly Cys Pro Val Asp Leu Glu Asp Ile
 1010 1015 1020

Glu Phe Arg Tyr Arg Gln Arg Asp Ser Ala Arg Val Leu Arg Gly Val
 1025 1030 1035 1040

Ser Met Thr Ile Glu Pro Gly Gln Phe Val Ala Tyr Val Gly Ala Ser
 1045 1050 1055

Gly Cys Gly Lys Ser Thr Leu Ile Ala Leu Ser Glu Arg Phe Tyr Asp
 1060 1065 1070

Pro Thr Ser Gly Arg Ile Ser Phe Ala His Glu Asn Ile Ala Glu Met
 1075 1080 1085

Ser Pro Arg Leu Tyr Arg Gly His Met Ser Leu Val Gln Gln Glu Pro
 1090 1095 1100

Thr Leu Tyr Gln Gly Ser Val Arg Glu Asn Val Thr Leu Ala Leu Glu
 1105 1110 1115 1120

Ala Glu Leu Ser Glu Glu Leu Cys Gln Gly Arg Leu Pro Ala Arg Pro
 1125 1130 1135

Met Leu Trp Ile Leu Ser Ser Leu Tyr Gln Lys Ala Leu Lys Arg Leu
 1140 1145 1150

Ala Ala Gln Arg Gly Met Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile
 1155 1160 1165

Ala Ile Ala Arg Ala Leu Ile Arg Asn Pro Lys Leu Leu Leu Leu Asp
1170 1175 1180

Glu Ala Thr Ser Ala Leu Asp Thr Gln Ser Glu Arg Leu Val Gln Ala
1185 1190 1195 1200

Ala Leu Asp Glu Ala Ser Thr Ser Arg Thr Thr Ile Ala Val Ala His
1205 1210 1215

Arg Leu Ser Thr Ile Arg Asn Val Asp Val Ile Phe Val Phe Ala Asn
1220 1225 1230

Gly Arg Ile Ala Glu Thr Gly Thr His Ala Glu Leu Gln Arg Leu Arg
1235 1240 1245

Gly Arg Tyr Tyr Glu Met Cys Leu Ala Gln Ser Leu Asp Gln Ala
1250 1255 1260

1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500